



OICE

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## RAW SEQUENCE LISTING

DATE: 03/04/2002

PATENT APPLICATION: US/10/077,111

TIME: 14:52:07

Input Set : A:\30534111.app

Output Set: N:\CRF3\03042002\J077111.raw

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3 <110> APPLICANT: Todderud, C. Gordon
4     Finger, Joshua N.
5     Rillema, Jill
7 <120> TITLE OF INVENTION: TBA
9 <130> FILE REFERENCE: 3053-4114US2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/077,111
C--> 12 <141> CURRENT FILING DATE: 2002-02-15
14 <150> PRIOR APPLICATION NUMBER: 60/294,181
15 <151> PRIOR FILING DATE: 2001-05-29
17 <150> PRIOR APPLICATION NUMBER: 60/269,366
18 <151> PRIOR FILING DATE: 2001-02-16
20 <160> NUMBER OF SEQ ID NOS: 25
22 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <211> LENGTH: 1818
26 <212> TYPE: DNA
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32 caggtctgtt ttcttcaa atagaacatg gtgaaactga ttacacatt agctgatcat 180
33 ggtgacgatg tcaactgtct tgcttctctc ttttccctct tggctacttg ctcttggac 240
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35 ttccatacct atgctgtcca ctgtctgtgt ttctccctct caggacatat tttggcatcg 360
36 tgttcaacag atggtacacc tgtctatgga aatactgaaa atggacagat gctggcagtg 420
37 atggaacagc ctagtggcag cctgtgagg gtttgccagt ttcccccaga ctccacgtgt 480
38 ttggcatcag ggcagctga tggaaactgt gttttgtgga atgcacagtc atacaaatta 540
39 tatagatgtg gtagtgtaa agatggctcc ttggcggcat gtgcatttct tctaatgga 600
40 agcttctttg tcaactggctc ctcatgttgt gatttaacag tgtgggatga taaaatgagg 660
41 tgtctgcata gtgaaaaagc acatgatctt ggaattacct gctgcgattt ttcttcacag 720
42 ccagtttctg atggagaaca aggtcttcag ttttttcgac tggcatcatg tggtcaggat 780
43 tgccaagtc aattttggat tgtttctttt acccatatct taggttttga attaaaatat 840
44 aaaagtacac tgagtgggca ctgtgtctct gttctggctt gtgcttttct ccatgatggg 900
45 cagatgctag tctcagggtc agtggataag tctgtcatag tatatgatac taatactgag 960
46 aatatacttc acacattgac tcagcacacc aggtatgtca caacttgtgc ttttgcaact 1020
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48 ctggaacac tttgccaagc aaggcgcaca gaacatcagc tgaagcaatt taccgaagat 1140
49 tggtcagagg aggatgtctc aacatggctt tgtgcacaag atttaaaaga tcttgttgtt 1200
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53 ataactagag aacttatgaa agatccggctc atgcgcatcag atggctattc atatgaaaag 1440
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55 ctctcttcag cggtaacttac accaaatagg actctgaaaa tggccatcaa tagatggctg 1560
56 gagacacacc aaaagtaaaa ttgttgatat tgtattatatt atattttcag tgatctcatt 1620
57 tgaatgattt ataggtaaact actaatcaga cattattaaa agcaaaacag gaaaaagga 1680
58 aacttcttaa atttagttac ctataaaaaat tgtcaatttt cattctttta aaaacacatg 1740
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63 <212> TYPE: PRT
64 <213> ORGANISM: HUMAN
65 <400> SEQUENCE: 2
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70 1 5 10 15
71 Cys Cys Ala Phe Ser Phe Ser Leu Leu Ala Thr Cys Ser Leu Asp Lys
72 20 25 30
73 Thr Ile Arg Leu Tyr Ser Leu Arg Asp Phe Thr Glu Leu Pro His Ser
74 35 40 45
75 Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys Cys Phe Ser Pro
76 50 55 60
77 Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly Thr Thr Val Leu
78 65 70 75 80
79 Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met Glu Gln Pro Ser
80 85 90 95
81 Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp Ser Thr Cys Leu
82 100 105 110
83 Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp Asn Ala Gln Ser
84 115 120 125
85 Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly Ser Leu Ala Ala
86 130 135 140
87 Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr Gly Ser Ser Cys
88 145 150 155 160
89 Gly Asp Leu Thr Val Trp Asp Asp Lys Met Arg Cys Leu His Ser Glu
90 165 170 175
91 Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe Ser Ser Gln Pro
92 180 185 190
93 Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg Leu Ala Ser Cys
94 195 200 205
95 Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser Phe Thr His Ile
96 210 215 220
97 Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser Gly His Cys Ala
98 225 230 235 240
99 Pro Val Leu Ala Cys Ala Phe Ser His Asp Gly Gln Met Leu Val Ser
100 245 250 255
101 Gly Ser Val Asp Lys Ser Val Ile Val Tyr Asp Thr Asn Thr Glu Asn
102 260 265 270
103 Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val Thr Thr Cys Ala
104 275 280 285
105 Phe Ala Pro Asn Thr Leu Leu Leu Ala Thr Gly Ser Met Asp Lys Thr
106 290 295 300

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126 Val Asn Ile Trp Gln Phe Asp Leu Glu Thr Leu Cys Gln Ala Arg Arg
127 305 310 315 320
129 Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp Ser Glu Glu Asp
130 325 330 335
132 Val Ser Thr Trp Leu Cys Ala Gln Asp Leu Lys Asp Leu Val Gly Ile
133 340 345 350
135 Phe Lys Met Asn Asn Ile Asp Gly Lys Glu Leu Leu Asn Leu Thr Lys
136 355 360 365
138 Glu Ser Leu Ala Asp Asp Leu Lys Ile Glu Ser Leu Gly Leu Arg Ser
139 370 375 380
141 Lys Val Leu Arg Lys Ile Glu Glu Leu Arg Thr Lys Val Lys Ser Leu
142 385 390 395 400
144 Ser Ser Gly Ile Pro Asp Glu Phe Ile Cys Pro Ile Thr Arg Glu Leu
145 405 410 415
147 Met Lys Asp Pro Val Ile Ala Ser Asp Gly Tyr Ser Tyr Glu Lys Glu
148 420 425 430
150 Ala Met Glu Asn Trp Ile Ser Lys Lys Lys Arg Thr Ser Pro Met Thr
151 435 440 445
153 Asn Leu Val Leu Pro Ser Ala Val Leu Thr Pro Asn Arg Thr Leu Lys
154 450 455 460
156 Met Ala Ile Asn Arg Trp Leu Glu Thr His Gln Lys
157 465 470 475

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160 &lt;210&gt; SEQ ID NO: 3

161 &lt;211&gt; LENGTH: 1553

162 &lt;212&gt; TYPE: DNA

163 &lt;213&gt; ORGANISM: HUMAN

165 &lt;400&gt; SEQUENCE: 3

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167 gatcccgccg gcccccgcgc ctgcaggtct tttttcttca aataaagaac atggtgaaac 120
168 tgattcacac attagctgat catggtgacg atgtcaactg ctgtgccttc tctttttccc 180
169 tcttggtcac ttgctccttg gacaaaacaa ttgccttgta ctgttaactg gactttactg 240
170 aactgcacac ttctccattg aagtttccata cctatgctgt ccactgctgc tgtttctccc 300
171 cttcaggaca tattttgcca tcgtgttcaa cagatggtac cactgtccta tgggaatactg 360
172 aaaatggaca gatgctggca gtgatggaac agcctagtgg cagccctgtg agggtttgcc 420
173 agttttcccc agactccacg tgtttggcat caggggcagc tgatggaact gtggttttgt 480
174 ggaatgcaca gtcatacaaa ttatatagat gtggtagtgt taaagatggc tcttgggcgg 540
175 catgtgcatt ttctcctaatt ggaagcttct ttgtcactgg ctctcctatg ggtgatttaa 600
176 cagtgtggga tgataaaatg aggtgtctgc atagtgaaaa agcacatgat cttggaatta 660
177 cctgctgcga tttttcttca cagccagttt ctgatggaga acaaggctct cagttttttc 720
178 gactggcacc atgtggctcag gattgccaag tcaaaatttg gattgtttct tttaccata 780
179 tcttaggttt tgaattaaaa tataaaagta cactgagtgg gcactgtgct cctgttctgg 840
180 cttgtgcttt tcccgtgat gggcagatgc tagtctcagg gtcagtggat aagtctgtca 900
181 tagtatatga tactaatact gagaatatac ttccacacatt gactcagcac accaggtatg 960
182 tcacaacttg tgtttttgca cctaataccc ttttacttgc tactggttca atggacaaaa 1020
183 cagtgaacat ctggcaattt gacctggaaa cactttgccg agcaaggcgc acagaacatc 1080
184 agctgaagca atttaccgaa gattggctcag aggaggatgt ctcaacatgg ctttgtgcac 1140
185 aagatttaaa agatcttggt ggtattttca agatgaataa cattgatgga aaagaactgt 1200
186 tgaatcttac aaaagaaagt ctggtctgat atttgaaaat tgaatctcta ggactgcgta 1260
187 gtaaagtgtc gaggaaaatt gaagagctca ggaccaaggt taaatccctt tcttcaggaa 1320

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189 cagatggcta ttcatatgaa aaggaagcaa tggaaaattg gatcagcaaa aagaaaagta 1440
190 caagtcccat gacaaatctt gttcttcttt cagcggtaact tacaccaaatt aggactctga 1500
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203 Leu Glu Gly Gly Ser Arg Ala Pro Pro Leu Leu Gln Ala Val Phe Leu
204 20 25 30
206 Gln Ile Lys Asn Met Val Lys Leu Ile His Thr Leu Ala Asp His Gly
207 35 40 45
209 Asp Asp Val Asn Cys Cys Ala Phe Ser Phe Ser Leu Leu Ala Thr Cys
210 50 55 60
212 Ser Leu Asp Lys Thr Ile Arg Leu Tyr Ser Leu Arg Asp Phe Thr Glu
213 65 70 75 80
215 Leu Pro His Ser Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys
216 85 90 95
218 Cys Phe Ser Pro Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly
219 100 105 110
221 Thr Thr Val Leu Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met
222 115 120 125
224 Glu Gln Pro Ser Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp
225 130 135 140
227 Ser Thr Cys Leu Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp
228 145 150 155 160
230 Asn Ala Gln Ser Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly
231 165 170 175
233 Ser Leu Ala Ala Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr
234 180 185 190
236 Gly Ser Ser Cys Gly Asp Leu Thr Val Trp Asp Asp Lys Met Arg Cys
237 195 200 205
239 Leu His Ser Glu Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe
240 210 215 220
242 Ser Ser Gln Pro Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg
243 225 230 235 240
245 Leu Ala Ser Cys Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser
246 245 250 255
248 Phe Thr His Ile Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser
249 260 265 270
251 Gly His Cys Ala Pro Val Leu Ala Cys Ala Phe Ser Arg Asp Gly Gln
252 275 280 285
254 Met Leu Val Ser Gly Ser Val Asp Lys Ser Val Ile Val Tyr Asp Thr
255 290 295 300
257 Asn Thr Glu Asn Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val
258 305 310 315 320

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DATE: 03/04/2002

TIME: 14:52:07

Input Set : A:\30534111.app

Output Set: N:\CRF3\03042002\J077111.raw

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260 Thr Thr Cys Ala Phe Ala Pro Asn Thr Leu Leu Leu Ala Thr Gly Ser
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263 Met Asp Lys Thr Val Asn Ile Trp Gln Phe Asp Leu Glu Thr Leu Cys
264                340                345                350
266 Gln Ala Arg Arg Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp
267                355                360                365
269 Ser Glu Glu Asp Val Ser Thr Trp Leu Cys Ala Gln Asp Leu Lys Asp
270                370                375                380
272 Leu Val Gly Ile Phe Lys Met Asn Asn Ile Asp Gly Lys Glu Leu Leu
273 385                390                395                400
275 Asn Leu Thr Lys Glu Ser Leu Ala Asp Asp Leu Lys Ile Glu Ser Leu
276                405                410                415
278 Gly Leu Arg Ser Lys Val Leu Arg Lys Ile Glu Glu Leu Arg Thr Lys
279                420                425                430
281 Val Lys Ser Leu Ser Ser Gly Ile Pro Asp Glu Phe Ile Cys Pro Ile
282                435                440                445
284 Thr Arg Glu Leu Met Lys Asp Pro Val Ile Ala Ser Asp Gly Tyr Ser
285                450                455                460
287 Tyr Glu Lys Glu Ala Met Glu Asn Trp Ile Ser Lys Lys Lys Arg Thr
288 465                470                475                480
290 Ser Pro Met Thr Asn Leu Val Leu Pro Ser Ala Val Leu Thr Pro Asn
291                485                490                495
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294                500                505                510

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300 &lt;210&gt; SEQ ID NO: 5

301 &lt;211&gt; LENGTH: 630

302 &lt;212&gt; TYPE: DNA

303 &lt;213&gt; ORGANISM: HUMAN

305 &lt;220&gt; FEATURE:

306 &lt;223&gt; OTHER INFORMATION: 630 bp partial nucleic acid sequence of human

307 RET16 cDNA

309 &lt;400&gt; SEQUENCE: 5

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312 ctccacacat tgaactcagc caccaggtat gtcacaactt gtgcttttgc acctaatacc 180
313 cttttacttg ctactgggtc aatggacaaa acagtgaaca tctggcaatt tgacctggaa 240
314 acactttgac aagcaaggcg cacagaacat cagctgaagg aatttaccga agattggcca 300
315 gaggaggatg tctcaacatg gctttgtgca caagatttaa aagatcttgt tggatttttc 360
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318 aggaaccaag ttaaatccct ttcttcagga attctgatg aatttatatg tccaataact 540
319 agagaactta tgaaagatcc ggtcctcaca tcagatggct attcatatga aaaggaagca 600
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325 &lt;212&gt; TYPE: DNA

326 &lt;213&gt; ORGANISM: MOUSE

328 &lt;400&gt; SEQUENCE: 6

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VERIFICATION SUMMARY

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DATE: 03/04/2002

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date